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AMENDMENTS TO THE CLAIMS:

Listing of Claims:

1. (currently amended) A method for comparing a first microarray spot A with a second microarray spot B comprising:

providing a first plurality of intensity values (S_i^A) for [said] a first microarray spot A and a second plurality of intensity values (S_k^B) for a second microarray spot B, wherein i denotes a ith pixel for spot A and k denotes a kth pixel for spot B and wherein the intensity values indicate nucleic acid hybridization;

calculating a p value using Wilcoxon's rank test, wherein p value is for a null hypothesis that $\theta=0$ and an alternative hypothesis that said $\theta>0$, wherein θ is a test statistic for intensity difference between said plurality and said second plurality; and

indicating said first microarray spot is different from said second microarray spot if said p value is greater than a significance level.

2. (original)   The method of Claim 1 wherein said testing statistic is *median (S_i^A)- median (S_k^B)*.

3. (original)   The method of Claim 2 wherein said significance level is 0.05.

4. (original)   The method of Claim 1 wherein said first microarray spot and second microarray spot are nucleic acid spots.

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5. (original)   The method of Claim 4 wherein said nucleic acid spots are among at least 100 nucleic acid spots on a substrate.

6. (original)   The method of Claim 5 wherein said nucleic acid spots are among at least 1000 spots on a substrate.

7. (original)   The method of Claim 6 wherein said nucleic acid spots are cDNA spots.

8. (original)   The method of Claim 7 wherein said nucleic acid spots are oligonucleotide spots.

9. (original)   The method of Claim 1 further comprising step of combining first plurality and second plurality of intensity values if said p-value is greater than a significance level.

10. (currently amended)   A computer software product for comparing first microarray spot A with a second microarray spot B comprising:

computer program code for inputing a first plurality of intensity values (S_i^A) for [said] a first microarray spot A and a second plurality of intensity values (S_k^B) for a second microarray spot B, wherein i denotes a ith pixel for spot A and k denotes a kth pixel for spot B and wherein the intensity values indicate nucleic acid hybridization;

computer program code for calculating a p value using Wilcoxon's rank test, wherein p value is for a null hypothesis that $\theta=0$ and an alternative hypothesis that said

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$\theta>0$, wherein θ is a test statistic for intensity difference between said plurality and said second plurality;

computer program code for indicating said first microarray spot is different from said second microarray spot if said p value is greater than a significance level; and

a computer readable media for storing said computer program codes.

11. (original)   The computer program product of Claim 10 wherein said testing statistic is *median (S_i^A)-median (S_k^B)*.

12. (original)   The computer software product of Claim 11 wherein said significance level is 0.05.

13. (original)   The computer software product of Claim 11 further comprising computer program code for accepting user's input or selection of said significance level.

14. (original)   The computer software product of Claim 11 wherein said first microarray spot and second microarray spot are nucleic acid spots.

15. (original)   The computer software product of Claim 14 wherein said nucleic acid spots are among at least 100 nucleic acid spots on a substrate.

16. (original)   The computer software product of Claim 15 wherein said nucleic acid spots are among at least 1000 spots on a substrate.

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17. (original)   The computer software product of Claim 16 wherein said nucleic acid spots are cDNA spots.

18. (original)   The computer software product of Claim 16 wherein said nucleic acid spots are oligonucleotide spots.

19. (previously presented)   The computer software product of Claim 10 further comprising a computer program code for combining first plurality and second plurality of intensity values if said p-value is greater than a significance level.

20. (original)   The computer software product of Claim 19 wherein said significance level is 0.5.

21. (currently amended)   A system for comparing nucleic acid probes comprising:

a processor; and

a memory being coupled with a processor, the memory storing a plurality machine instructions that cause the processor to perform a plurality of logical steps when implemented by the processor, said logical steps including:

inputing a first plurality of intensity values (S_i^A) for a first microarray spot A and a second plurality of intensity values (S_k^B) for a second microarray spot B, wherein i denotes a ith pixel for spot A and k denotes a kth pixel for spot B and wherein the intensity values indicate nucleic acid hybridization;

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calculating a p value using Wilcoxon's rank test, wherein p value is for a null

hypothesis that $\theta=0$ and an alternative hypothesis that said $\theta>0$, wherein θ is a test

statistic for intensity difference between said plurality and said second plurality; and

indicating said first microarray spot is different from said second microarray spot

if said p value is greater than a significance level.

22. (original)   The system of Claim 21 wherein said testing statistic is *median (S_i^A)-*

median (S_k^B).

23. (original)   The system of Claim 22 wherein said significance level is 0.05.

24. (original)   The system of Claim 22 wherein said steps further comprise accepting

user's input or selection of said significance level.

25. (original)   The system of Claim 21 wherein said first microarray spot and second

microarray spot are nucleic acid spots.

26. (original)   The system of Claim 25 wherein said nucleic acid spots are among at least

100 nucleic acid spots on a substrate.

27. (original)   The system of Claim 26 wherein said nucleic acid spots are among at least

1000 spots on a substrate.

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28. (original)   The system of Claim 27 wherein said nucleic acid spots are cDNA spots.

29. (original)   The system of Claim 27 wherein said nucleic acid spots are oligonucleotide spots.

30. (original)   The system of Claim 21 further comprise combining first plurality and second plurality of intensity values if said p-value is greater than a significance level.

31. (original)   The system of Claim 30 wherein said significance level is 0.5.

32. (withdrawn)   A method for determining whether a transcript is present in a biological sample comprising:

provided a plurality of perfect match pixel intensity values (PM_{ij}) and mismatch pixel intensity values (MM_{ik}) for the transcript, wherein said PM_{ij} is the pixel intensity for the perfect match probe i and pixel j and MM_{ik} is the pixel intensity value for mismatch probe i and pixel k;

calculating a p-value using one-sided Wilcoxon's rank sum test, wherein the p-value is for a null hypothesis that ($median(PM_{ij})$-$median(MM_{ik})$=a threshold value and an alternative hypothesis that said ($median(PM_{ij})$-$median(MM_{ik})$>said threshold value; and

indicating whether said transcript is present based upon said p-value.

33. (withdrawn)   The method of Claim 32 wherein the threshold value is zero.

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34.   (withdrawn) The method of Claim 32 wherein the threshold value is calculated

using: $\tau = c\sqrt{median\ (PM_i)}$ wherein said c is a constant.

35.   (withdrawn) The method of Claim 32 wherein the threshold value is calculated

using: $\tau = c_1\sqrt{median\ (PM_i)}$ wherein said c is a constant.

36.   (withdrawn) The method of Claim 32 wherein said step of indicating comprises

indicating said transcript is present if said p is smaller than a first significance

level (α_1).

37.   (withdrawn) The method of Claim 32 wherein said step of indicating comprises

indicating said transcript is absent if said p is greater or equal than a second

significance level (α_2).

38.   (withdrawn) The method of Claim 32 wherein said step of indicating comprises

indicating said transcript is marginally detected if $\alpha_1 \leq p < \alpha_2$.

39.   (withdrawn) A computer software product for determining whether a transcript is

present in a biological sample comprising:

        a computer program code for inputting a plurality of perfect match pixel

intensity values (PM_{ij}) and mismatch pixel intensity values (MM_{ik}) for the transcript,

wherein said PM_{ij} is the pixel intensity for the perfect match probe i and pixel j and

MM_{ik} is the pixel intensity value for mismatch probe i and pixel k;

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a computer software code for calculating a p-value using one-sided

Wilcoxon's rank sum test, wherein the p-value is for a null hypothesis that

$(median(PM_{ij})-median(MM_{ik})$=a threshold value and an alternative hypothesis that

said $(median(PM_{ij})-median(MM_{ik})$>said threshold value;

a computer software code for indicating whether said transcript is present

based upon said p-value; and

a computer readable media for storing said code.

40. (withdrawn) The computer software product of Claim 32 wherein said threshold

value is zero.

41. (withdrawn) The computer software product of Claim 32 wherein said threshold

value is calculated using: $\tau = c\sqrt{median\ (PM_i)}$ wherein said c is a constant.

42. (withdrawn) The computer software product of Claim 32 wherein said threshold

value is calculated using: $\tau = c_1\sqrt{median\ (PM_i)}$ wherein said c is a constant.

43. (withdrawn) The computer software product of Claim 32 wherein said computer

program code for indicating comprises computer software code for indicating that

said transcript is present if said p is smaller than a first significance level (α_1).

44. (withdrawn) The computer software product of Claim 32 wherein said computer

program code for indicating comprises computer software code for indicating that

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said transcript is absent if said p is greater or equal than a second significance level

(α_2).

45. (withdrawn) The computer software product of Claim 32 wherein said computer

program code for indicating comprises computer software code for indicating that

said transcript is marginally detected if $\alpha_1 \leq p < \alpha_2$.

46. (withdrawn) A system for comparing nucleic acid probes, comprising:

    a processor; and

    a memory being coupled to the processor, the memory storing a plurality

machine instructions that cause the processor to perform a plurality of logical

steps when implemented by the processor, said logical steps including:

    providing a plurality of perfect match pixel intensity values (PM_{ij}) and

mismatch pixel intensity values (MM_{ik}) for the transcript, wherein said PM_{ij} is the

pixel intensity for the perfect match probe i and pixel j and MM_{ik} is the pixel intensity

value for mismatch probe i and pixel k;

    calculating a p-value using one-sided Wilcoxon's rank sum test, wherein the

p-value is for a null hypothesis that ($median(PM_{ij})-median(MM_{ik})$=a threshold value

and an alternative hypothesis that said ($median(PM_{ij})-median(MM_{ik})$>said threshold

value; and

    indicating whether said transcript is present based upon said p-value.

47. (withdrawn) The system of Claim 46 wherein said threshold value is zero.

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48. (withdrawn) The system of Claim 47 wherein said threshold value is calculated using: $\tau = c\sqrt{median\ (PM_i)}$ wherein said c is a constant.

49. (withdrawn) The system of Claim 47 wherein said threshold value is calculated using: $\tau = c_1\sqrt{median\ (PM_i)}$ wherein said c is a constant.

50. (withdrawn) The system of Claim 46 wherein said step of indicating comprises indicating said transcript is present if said p is smaller than a first significance level (α_1).

51. (withdrawn) The system of Claim 50 wherein said step of indicating comprises indicating said transcript is absent if said p is greater or equal than a second significance level (α_2).

52. (withdrawn) The system of Claim 51 wherein said first significance (α_1) is smaller that said (α_2) and said step of indicating further comprises indicating said transcript is marginally detected if $\alpha_1 \leq p < \alpha_2$.

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